Exhibit 4

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program | blastn ▼ | Matrix | Not Applicable ▼ |

Parameters used in BLASTN program only:

Reward for a match: | 1   **Penalty for a mismatch:** | 2

☐ Use Mega BLAST   Strand option | Both strands ▼ |

Open gap | 5   and extension gap | 2   penalties

gap x_dropoff | 5 | expect | 10.0   word size | 11   Filter ☑   Align

Sequence 1 Enter accession or GI | 13027635 | or download from file

| Browse |

or sequence in FASTA format from: | 0   to: | 0

Sequence 2 Enter accession or GI | | or download from file

| Browse |

or sequence in FASTA format from: | 0   to: | 0

accggaagcgctccagacttggtcg

Align   Clear Input

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

Blast Result

Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]

Match: 1   Mismatch: 2   gap open: 5   gap extension: 2

x_dropoff: 50   expect: 10.00   wordsize: 11   Filter ☑   Align

Sequence 1	gi 13027635	Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1), mRNA	Length 2753
Sequence 2	lcl|seq_2		Length 25

No significant similarity was found